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Development and characterization of *in-silico* based EST-SSR markers in *Withania somnifera* & *Centella asiatica*

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Simple sequence repeat (SSR) markers obtained from expressed sequence tags (ESTs) are primary resources for gene discovery and mapping. The objectives of the work presented here are to develop EST based SSR markers in, *Withania somnifera* (Ashwagandha) and *Centella asiatica* (Indian pennywort) and to study it. Both the plants are medicinally important and contain several alkaloids, essential proteins and metabolites. In this study, a total of 742 *Withania somnifera* EST sequences & 4501 *Centella asiatica* EST sequences retrieved from dbEST database in FASTA format. (http://www.ncbi.nlm.nih.gov/nucest) on 17 June 2020, among these EST-SSRs, for *Withania somnifera* 335 SSRs identified 306 repeat units for mononucleotide repeats, 11 repeat units for dinucleotide repeats and 18 repeat units for trinucleotide repeats. Where, for *Centella asiatica*, there were 1389 SSRs identified 1122 repeat unit for mononucleotide repeats, 171 repeat units for dinucleotide repeats, 91 repeat units for trinucleotide repeats and 5 repeat units of tetranucleotide repeats. Out of these SSR-containing ESTs, a total of 25 primer pairs were designed for *Withania somnifera* and 50 primer pairs were developed for *Centella asiatica*. After the BLAST alignment of EST-SSR, their fuctions were identified, many of them were gene-related proteins and many of them were essential proteins, also many metabolically active proteins and enzymes were identified in both of the plant.

Key Words: Expressed Sequence Tag, Simple Sequence Repeats, *Withania somnifera* and *Centella asiatica.*

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